

Figure 1: Full-length Sequence of *C. pneumoniae* 76kDa Gene.

ataaaatctt taaaaacagg ctgcgcatat ttattagtga gagctttttt tttatttttt 60

ataataaaac taaaagattt ttattatttt ttgagttttt atg gtt aat cct att 115  
Met Val Asn Pro Ile  
1 5

ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat ctt 163  
Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp Leu  
10 15 20

tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa gct 211  
Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu Ala  
25 30 35

caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc gat 259  
Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr Asp  
40 45 50

tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc atg 307  
Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu Met  
55 60 65

agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct tct 355  
Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser Ser  
70 75 80 85

act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct acg 403  
Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro Thr  
90 95 100

cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca gct 451  
Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr Ala  
105 110 115

tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct gct 499  
Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala Ala  
120 125 130

ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg gct 547  
Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala Ala  
135 140 145

act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat gcc 595  
Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn Ala  
150 155 160 165

gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat gct 643  
Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr Ala  
170 175 180

tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc ttc 691  
Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser Phe  
185 190 195

Figure 1 (continued)

gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac aaa	739
Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn Lys	
200 205 210	
gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca ggg	787
Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro Gly	
215 220 225	
aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct aca	835
Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala Thr	
230 235 240 245	
gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat ttt	883
Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr Phe	
250 255 260	
gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat aac	931
Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn Asn	
265 270 275	
agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct aag	979
Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala Lys	
280 285 290	
aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att ctt	1027
Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile Leu	
295 300 305	
caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa aat	1075
Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys Asn	
310 315 320 325	
atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca gtt	1123
Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr Val	
330 335 340	
gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt tcc	1171
Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val Ser	
345 350 355	
atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg tct	1219
Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met Ser	
360 365 370	
ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat tct	1267
Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp Ser	
375 380 385	
caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa gcc	1315
Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys Ala	
390 395 400 405	
gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa gct	1363
Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys Ala	
410 415 420	

10014670-121401

Figure 1 (continued)

tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc aat	1411
Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu Asn	
425 430 435	
gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gtt cct	1459
Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val Pro	
440 445 450	
ccc gct gca gca agt tct ata ggg tca tct gta aaa cag ctt tac aag	1507
Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val Lys Gln Leu Tyr Lys	
455 460 465	
acc tca aaa tct aca ggt tct gat tat aaa aca cag ata tca gca ggt	1555
Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr Gln Ile Ser Ala Gly	
470 475 480 485	
tat gat gct tac aaa tcc atc aat gat gcc tat ggt agg gca cga aat	1603
Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ala Arg Asn	
490 495 500	
gat gcg act cgt gat gtg ata aac aat gta agt acc ccc gct ctc aca	1651
Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser Thr Pro Ala Leu Thr	
505 510 515	
cga tcc gtt cct aga gca cga aca gaa gct cga gga cca gaa aaa aca	1699
Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg Gly Pro Glu Lys Thr	
520 525 530	
gat caa gcc ctc gct agg gtg att tct ggc aat agc aga act ctt gga	1747
Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn Ser Arg Thr Leu Gly	
535 540 545	
gat gtc tat agt caa gtt tcg gca cta caa tct gta atg cag atc atc	1795
Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser Val Met Gln Ile Ile	
550 555 560 565	
cag tcg aat cct caa gcg aat aat gag gag atc aga caa aag ctt aca	1843
Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu Thr	
570 575 580	
tcg gca gtg aca aag cct cca cag ttt ggc tat cct tat gtg caa ctt	1891
Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln Leu	
585 590 595	
tct aat gac tct aca cag aag ttc ata gct aaa tta gaa agt ttg ttt	1939
Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu Phe	
600 605 610	
gct gaa gga tct agg aca gca gct gaa ata aaa gca ctt tcc ttt gaa	1987
Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe Glu	
615 620 625	
acg aac tcc ttg ttt att cag cag gtg ctg gtc aat atc ggc tct cta	2035
Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser Leu	
630 635 640 645	

## Figure 1 (continued)

tat tct ggt tat ctc caa taacaacacc taagtgttcg tttggagaga 2083  
Tyr Ser Gly Tyr Leu Gln  
650

ttattatgtg ctttggttaag gcctttggtg aggccttacc aacacactag aacgatcttc 2143

aataaataaa aga 2156

10014670-1940  
T04121-02CHT001

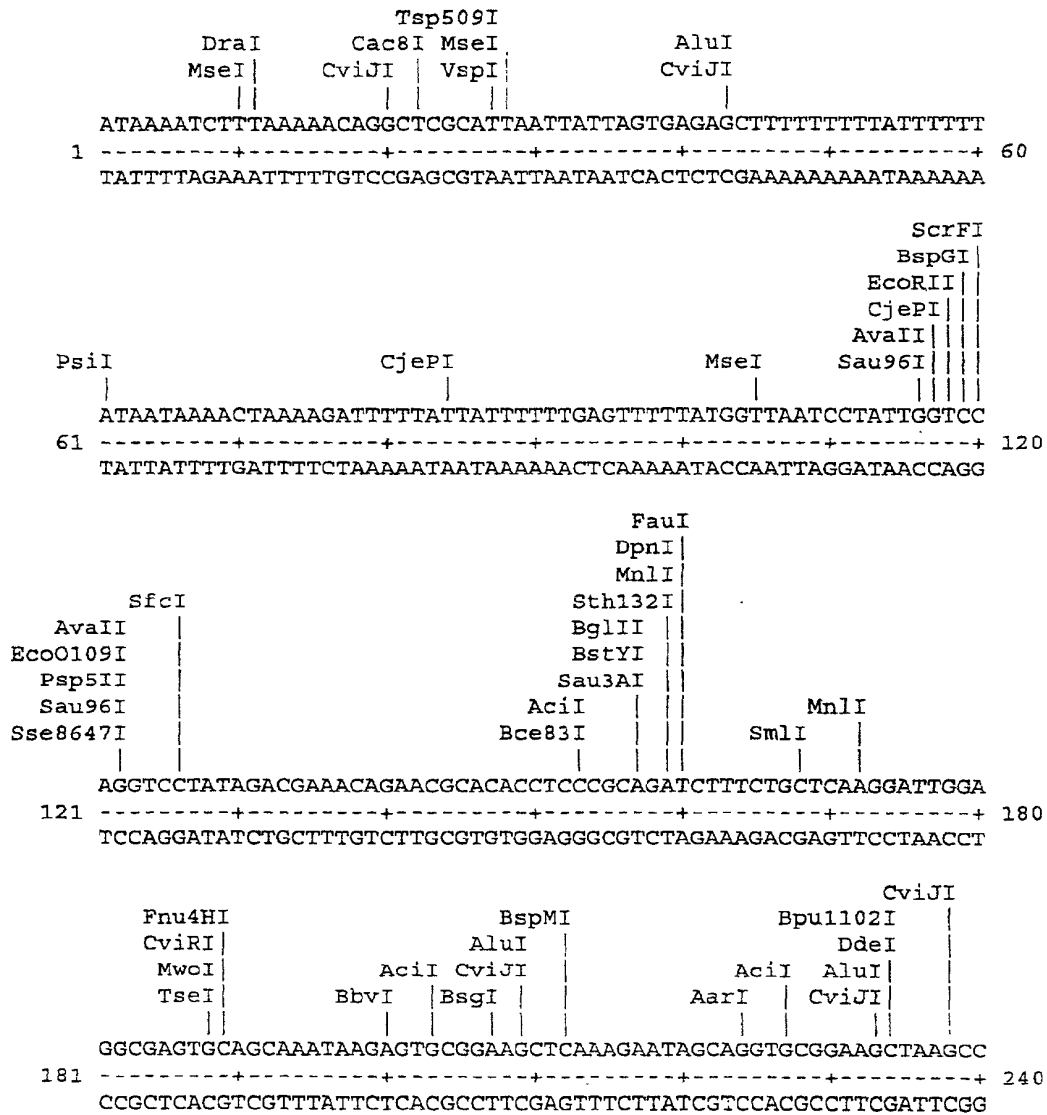
Figure 2: Restriction enzyme map of *C. pneumoniae* 76kDa gene.



Figure 2 (continued)

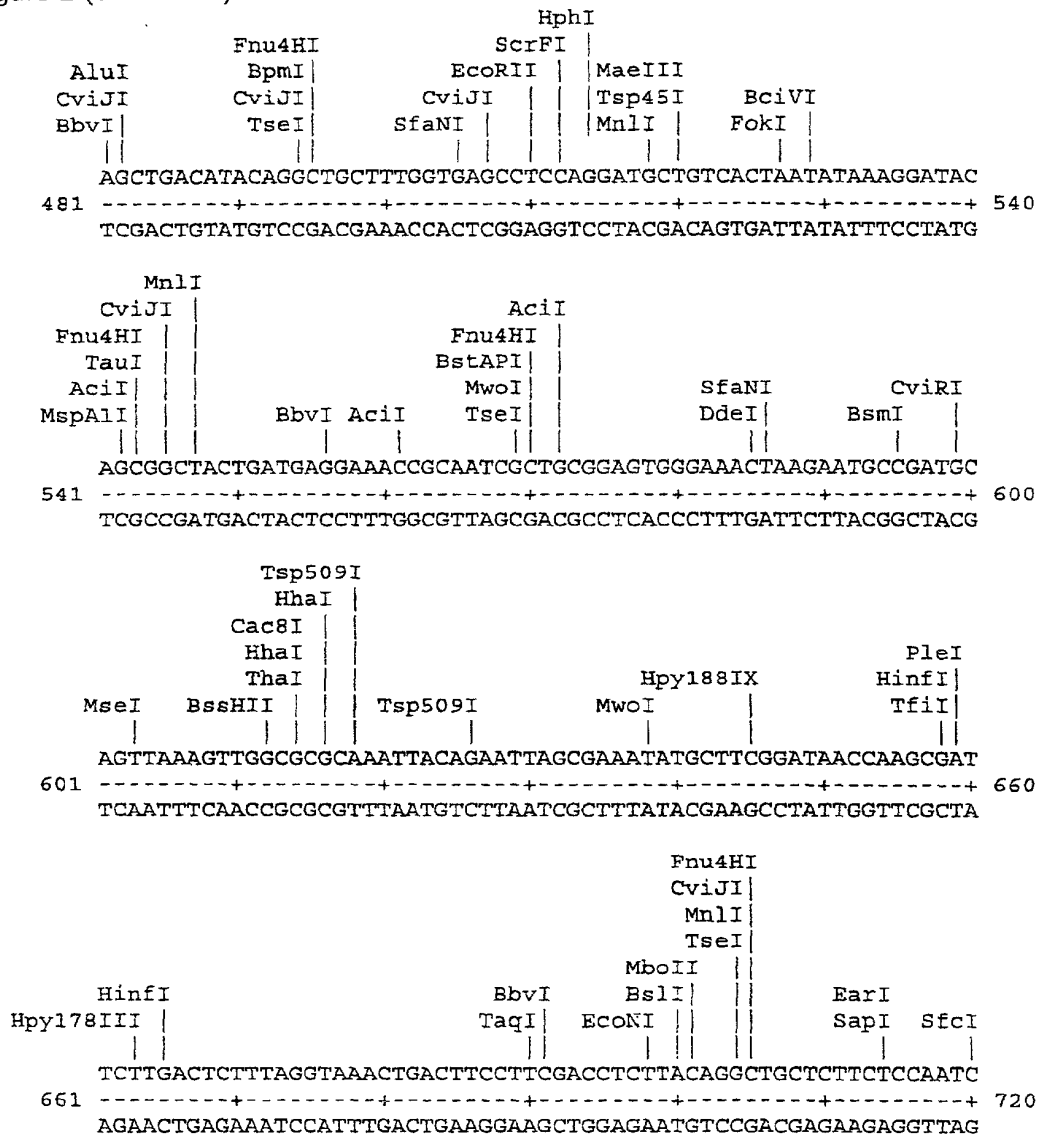


Figure 2 (continued)

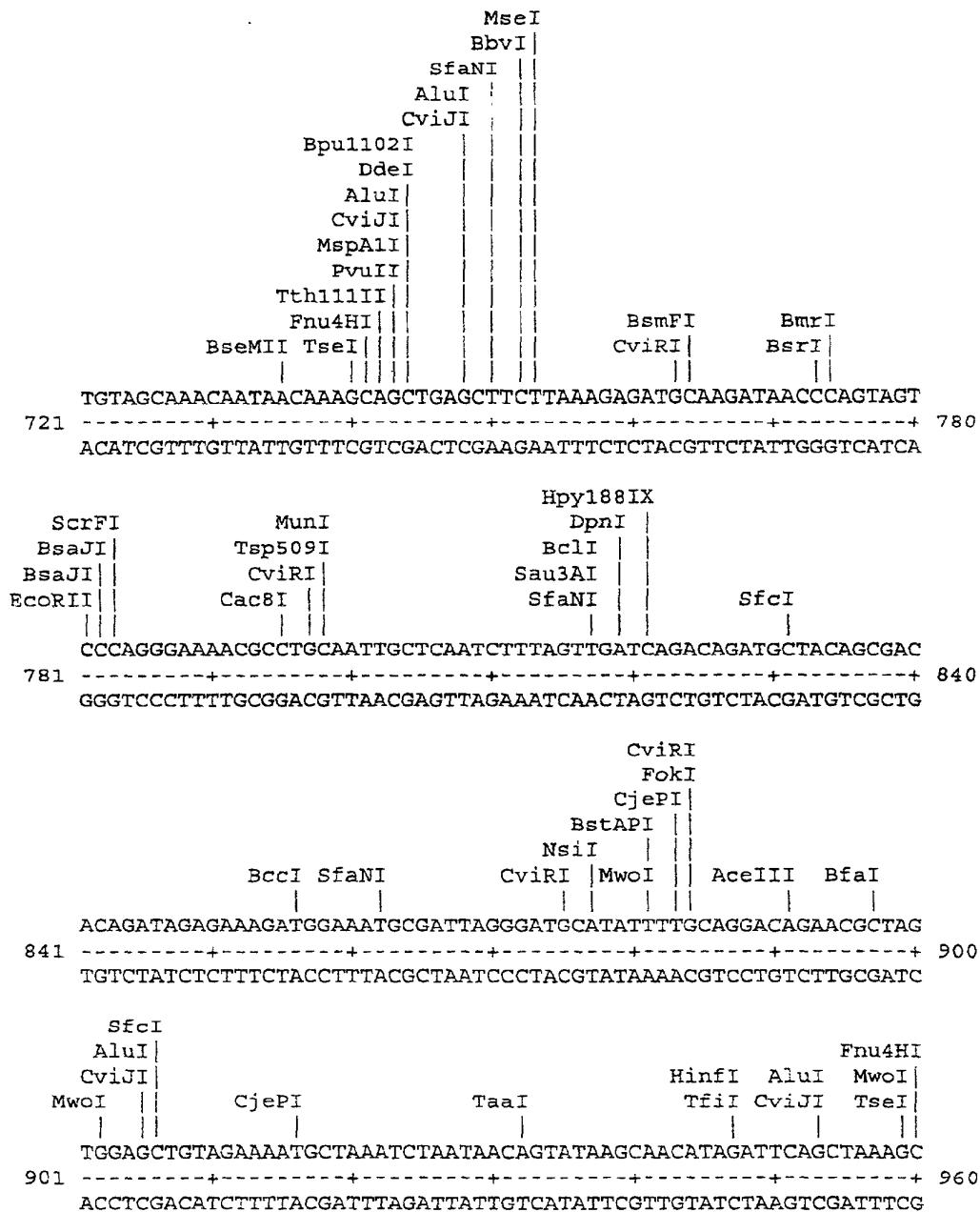
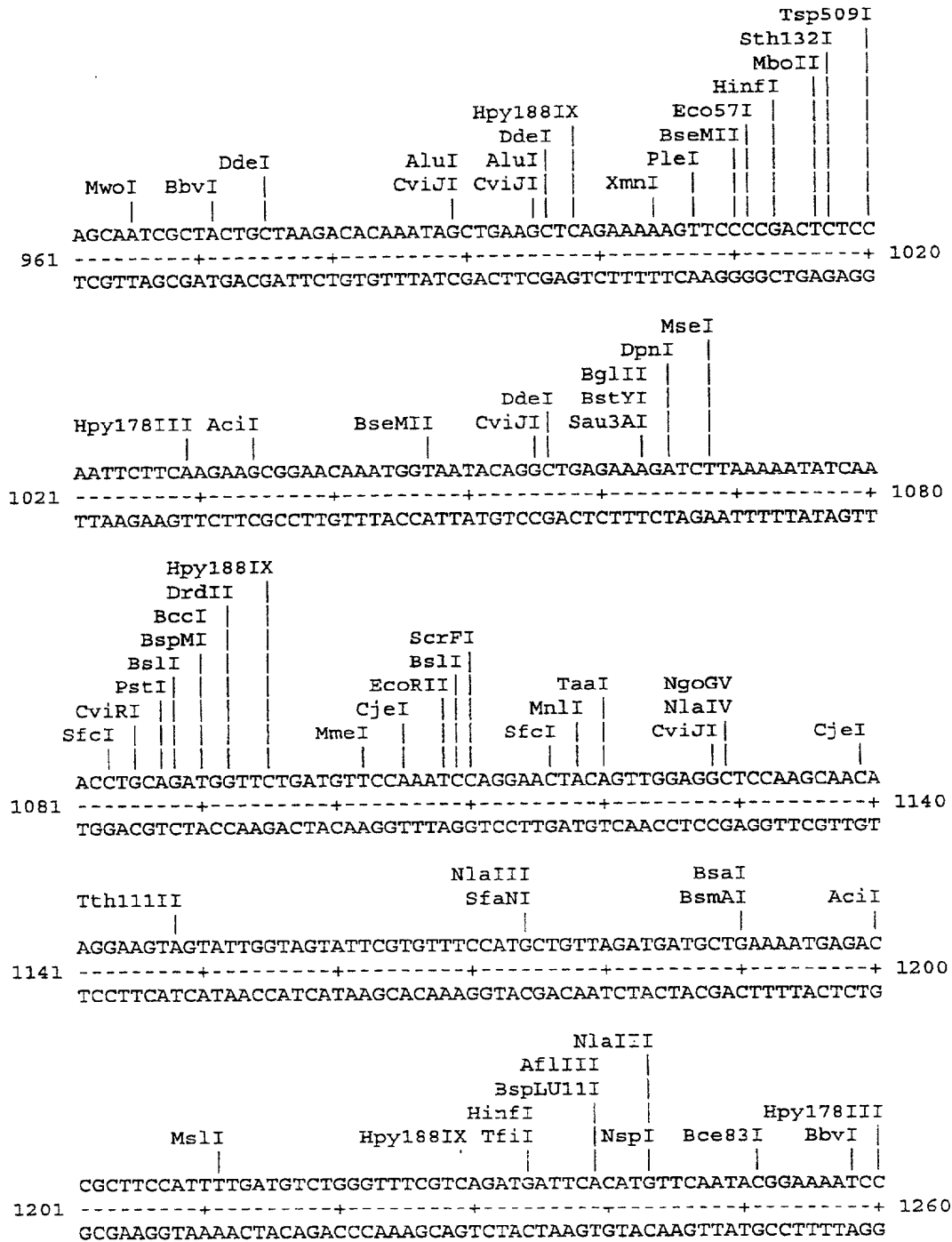




Figure 2 (continued)



[illegible]

Figure 2 (continued)

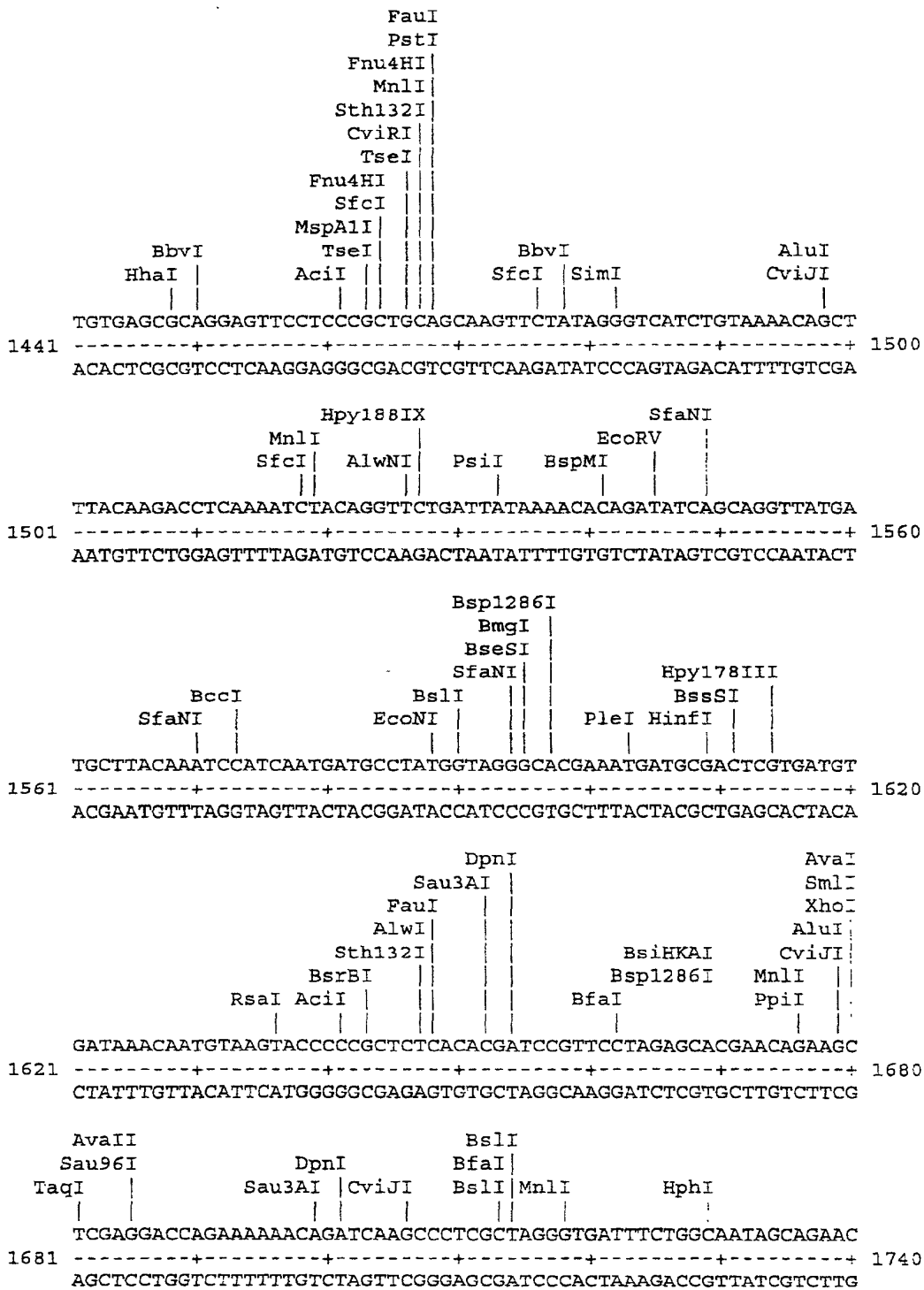


Figure 2 (continued)

Bce83I  
 DpnI  
 Sau3AI CviRI BsrI TaqI  
 SfcI FokI  
 TCTTGGAGATGTCTATAGTCAAGTTTCGGCACTACAATCTGTAATGCAGATCATCCAGTC  
 1741 -----+----- 1800  
 AGAACCTCTACAGATATCAGTTCAAAGCCGTGATGTTAGACATTACGTCTAGTAGGTCAG

CviJI  
 BsaXI  
 Hin4I  
 TspRI  
 AluI  
 Hpy188IX CviJI  
 BtsI  
 MaeIII  
 Tsp45I  
 HinfI TfiI SmlI MnlI MnlI Sau3AI DpnI BseRI HindIII  
 GAATCCTCAAGCGAATAATGAGGAGATCAGACAAAAGCTTACATCGGCAGTGACAAAGCC  
 1801 -----+----- 1860  
 CTTAGGAGTTCGCTTATTACTCCTCTAGTCTGTTTTCGAATGTAGCCGTCAGTCTTTTCGG

CviJI  
 MnlI  
 BslI  
 PflMI  
 TaaI  
 CviRI PleI HinfI  
 TCCACAGTTTGGCTATCCTTATGTGCAACTTTCTAATGACTCTACACAGAAGTTCATAGC  
 1861 -----+----- 1920  
 AGGTGTCAAACCGATAGGAATACAGCTTGAAAGATTACTGAGATGTGTCTTCAAGTATCG

Eco57I  
 AluI  
 AlwNI  
 CviJI  
 MspAII  
 PvuII  
 BfaI  
 DpnI Fnu4HI  
 TseI  
 Tth111III  
 Tsp509I Sau3AI AlwI BbvI  
 TAAATTAGAAAGTTTGTGTTGCTGAAGGATCTAGGACAGCAGCTGAAATAAAAGCACTTTC  
 1921 -----+----- 1980  
 ATTTAATCTTTCAAACAAACGACTTCCTAGATCCTGTGTCGACTTTATTTTCGTGAAAG

AlwNI  
 BspMI AarI CviJI  
 CTTTGAAACGAACTCCTTGTGTTTATTTCAGCAGGTGCTGGTCAATATCGGCTCTCTATATTC  
 1981 -----+----- 2040  
 GAAACTTTGCTTGAGGAACAAATAAGTCGTCCACGACCAGTTATAGCCGAGAGATATAAG

10014670-124401

Figure 2 (continued)

```

                MslI
                DdeI
                BsbI
                |
                |
                |
    TGGTTATCTCCAATAACAACACCTAAGTGTTCGTTTGGAGAGATTATTATGTGCTTGGT
2041 -----+-----+-----+-----+-----+ 2100
    ACCAATAGAGGTTATTGTTGTGGATTCACAAGCAAACCTCTCTAATAATACACGAAACCA

    MnlI
    CviJI |      CviJI      DpnI
    HaeI  |      HaeI      Sau3AI
    HaeIII|      HaeIII    MboII
    StuI  |      StuI      BsbI BfaI
    |      |      |      |
    AAGGCCTTTGTTGAGGCCTTACCAACACACTAGAACGATCTTCAATAAATAAAAGA
2101 -----+-----+-----+-----+-----+ 2156
    TTCCGGAAACAACCTCCGGAATGGTTGTGTGATCTTGCTAGAAGTTATTTATTTCT

```

10014670-13494

14/22

Figure 3: Sequence Containing Truncated Version of *C. pneumoniae* 76kDa Gene; (nucleotides 1 to 665 and 2122 to 2238 are unrelated to the 76kDa Gene).

```

atgacaaaaa aacattatgc ttgggttgta gaagggtatc tcaatcgttt gcctaaacag 60
ttttttgtga aatgtagtgt tgcgactggg aacacattcg ttccttcaga aacctccact 120
acagaaaaag ctgctacaaa cgctatgaaa taaaaatact gtgtttggca gtggctcgtc 180
ggaaagcata gtcagggttc ttggatcaat ggacagaaaa agcctctata tctttatgga 240
gctttcttaa tgaacccttt agcaaaggct acgaagacta cgttaaatgg aaaagaaaaac 300
ctagcttggt ttattggagg aactttaggg ggactcagaa aagctggaga ctggtctgcc 360
acagtacgtt atgagtatgt cgaagccttg tcggttcag aaatagatgt ttcagggatt 420
ggcctgggta atttattaaa gttttggttc gcccaagcaa ttgctgctaa ctatgaccc 480
aaagaggcta atgggtttac aaattataaa ggattttccg ctctatatat gtatggcatc 540
acagattctc tatcattcag agcttatggg gcttactcca aaccagcaaa cgataaactc 600
ggcagtgatt ttactttccg aaagtttgat ctaggataaa tttcagcgtt ttaagtcaaa 660
ttttaataaa atctttaaaa acaggetcgc attaattatt agtgagagct ttttttttat 720
ttttataaat aaaactaaaa gattttttatt attttttgag ttttt atg gtt aat cct 777
                                         Met Val Asn Pro
                                         1

att ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat 825
Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp
  5              10              15              20

ctt tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa 873
Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu
          25              30              35

gct caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc 921
Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr
          40              45              50

gat tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc 969
Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu
          55              60              65

atg agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct 1017
Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser
          70              75              80

tct act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct 1065
Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro
          85              90              95              100

```

10044570-12404

Figure 3 (continued)

acg cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca	1113
Thr Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr	
105 110 115	
gct tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct	1161
Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala	
120 125 130	
gct ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg	1209
Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala	
135 140 145	
gct act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat	1257
Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn	
150 155 160	
gcc gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat	1305
Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr	
165 170 175 180	
gct tgc gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc	1353
Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser	
185 190 195	
ttc gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac	1401
Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn	
200 205 210	
aaa gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca	1449
Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro	
215 220 225	
ggg aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct	1497
Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala	
230 235 240	
aca gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat	1545
Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr	
245 250 255 260	
ttt gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat	1593
Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn	
265 270 275	
aac agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct	1641
Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala	
280 285 290	
aag aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att	1689
Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile	
295 300 305	

Figure 3 (continued)

ctt caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa	1737
Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys	
310 315 320	
aat atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca	1785
Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr	
325 330 335 340	
gtt gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt	1833
Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val	
345 350 355	
tcc atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg	1881
Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met	
360 365 370	
tct ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat	1929
Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp	
375 380 385	
tct caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa	1977
Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys	
390 395 400	
gcc gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa	2025
Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys	
405 410 415 420	
gct tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc	2073
Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu	
425 430 435	
aat gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gta	2121
Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val	
440 445 450	
ctc ccg ctg cag caa gtt cta tgg atc cga gct cgg tac caa gct tac	2169
Leu Pro Leu Gln Gln Val Leu Trp Ile Arg Ala Arg Tyr Gln Ala Tyr	
455 460 465	
gta gaa caa aaa ctc atc tca gaa gag gat ctg aat agc gcc gtc gac	2217
Val Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp	
470 475 480	
cat cat cat cat cat cat tga	2238
His His His His His His	
485 490	



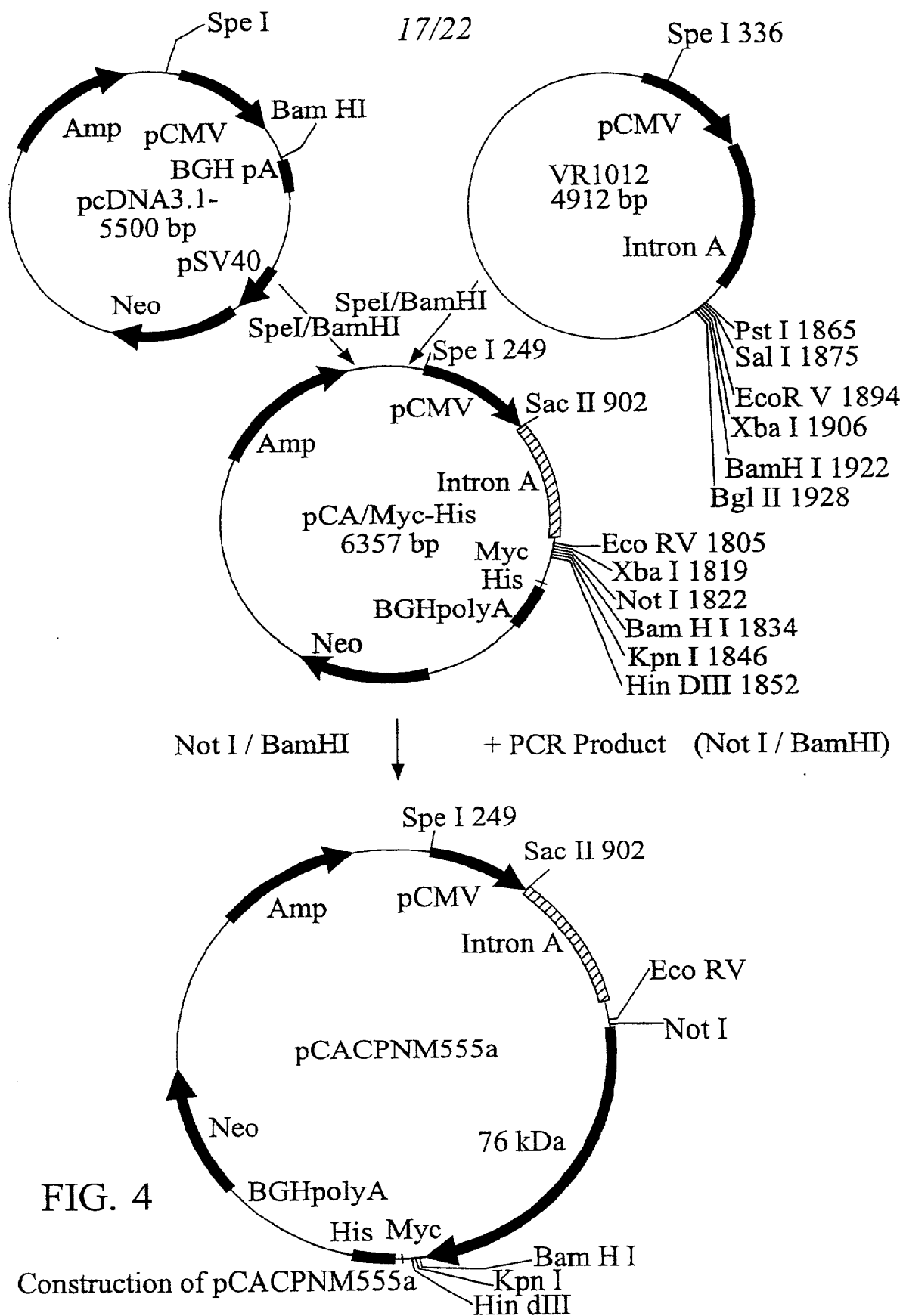


FIG. 4

Construction of pCACPNM555a

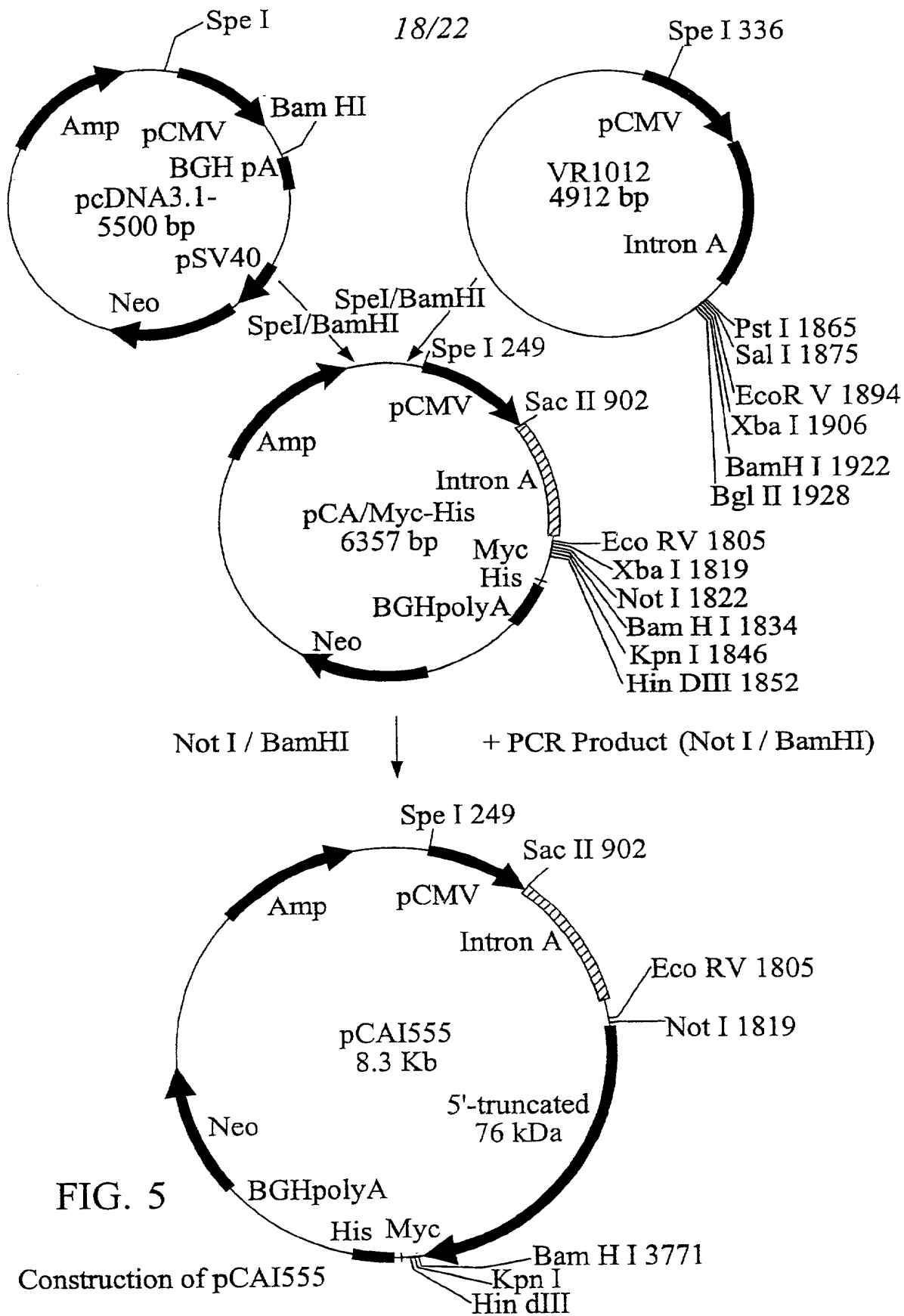


FIG. 5

Construction of pCAI555

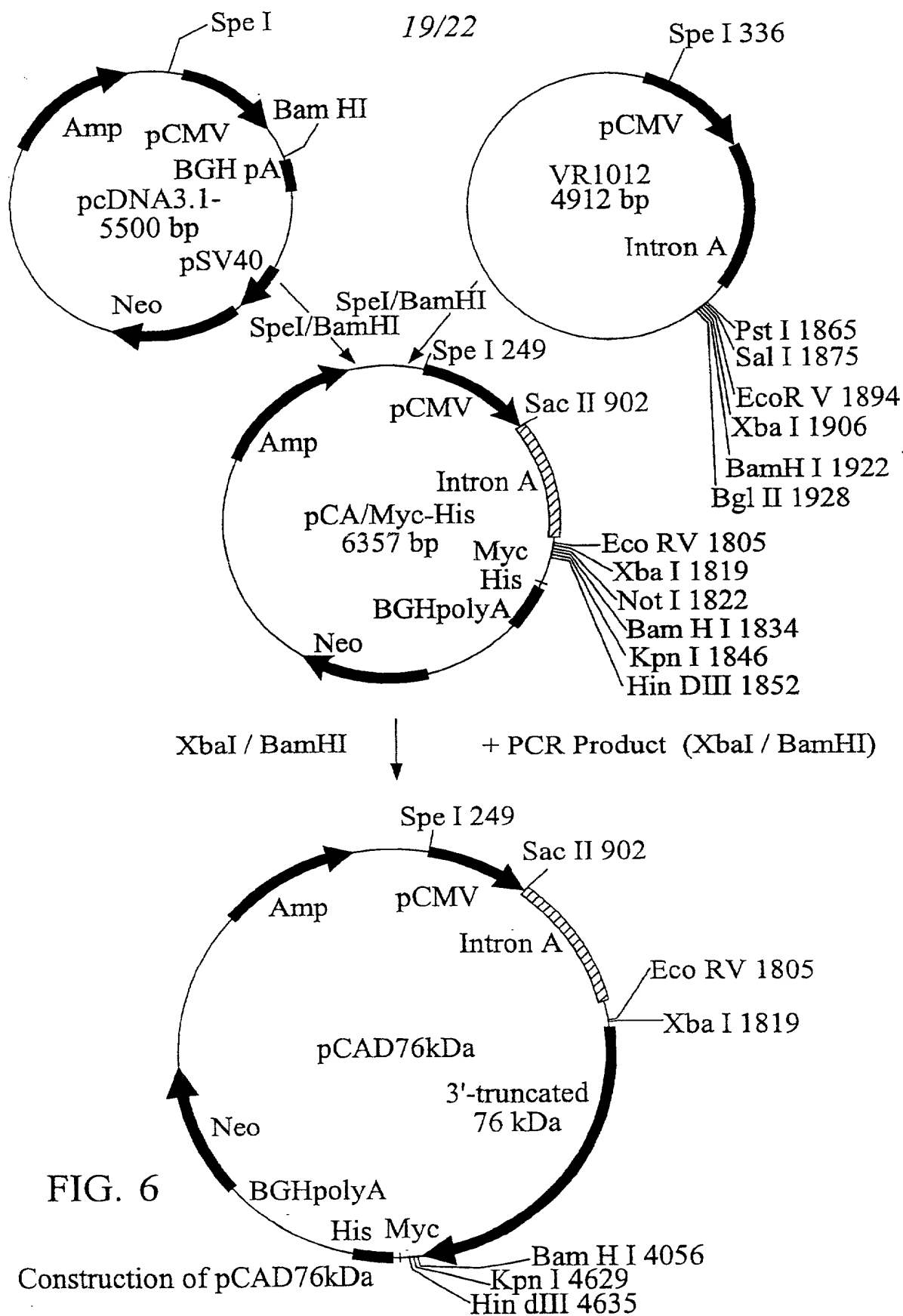


FIG. 6

Construction of pCAD76kDa

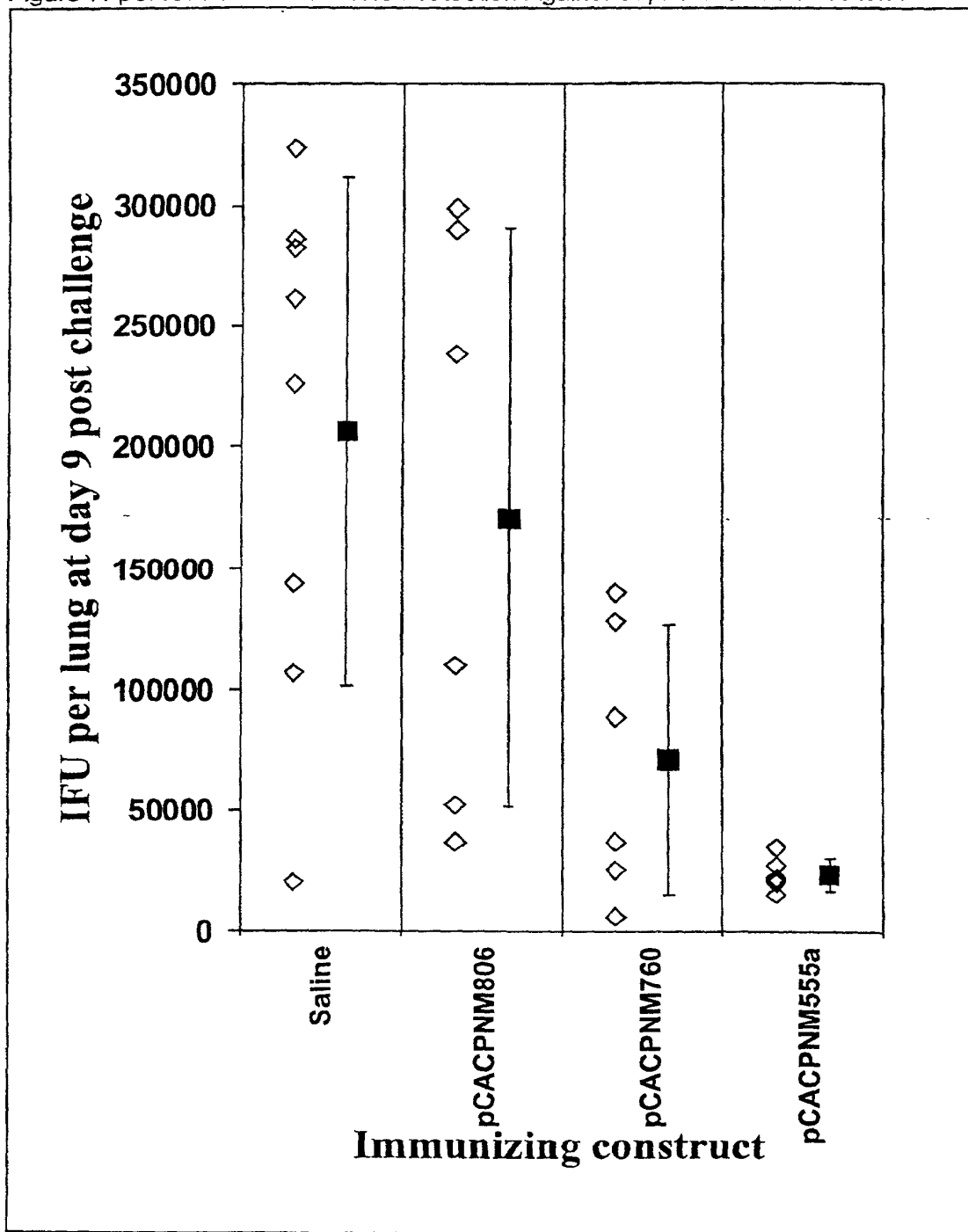
Figure 7: pCACPNM555a Confers Protection Against *C. pneumoniae* Infection .

Figure 8: pCAI555 Confers Protection Against *C. pneumoniae* Infection.

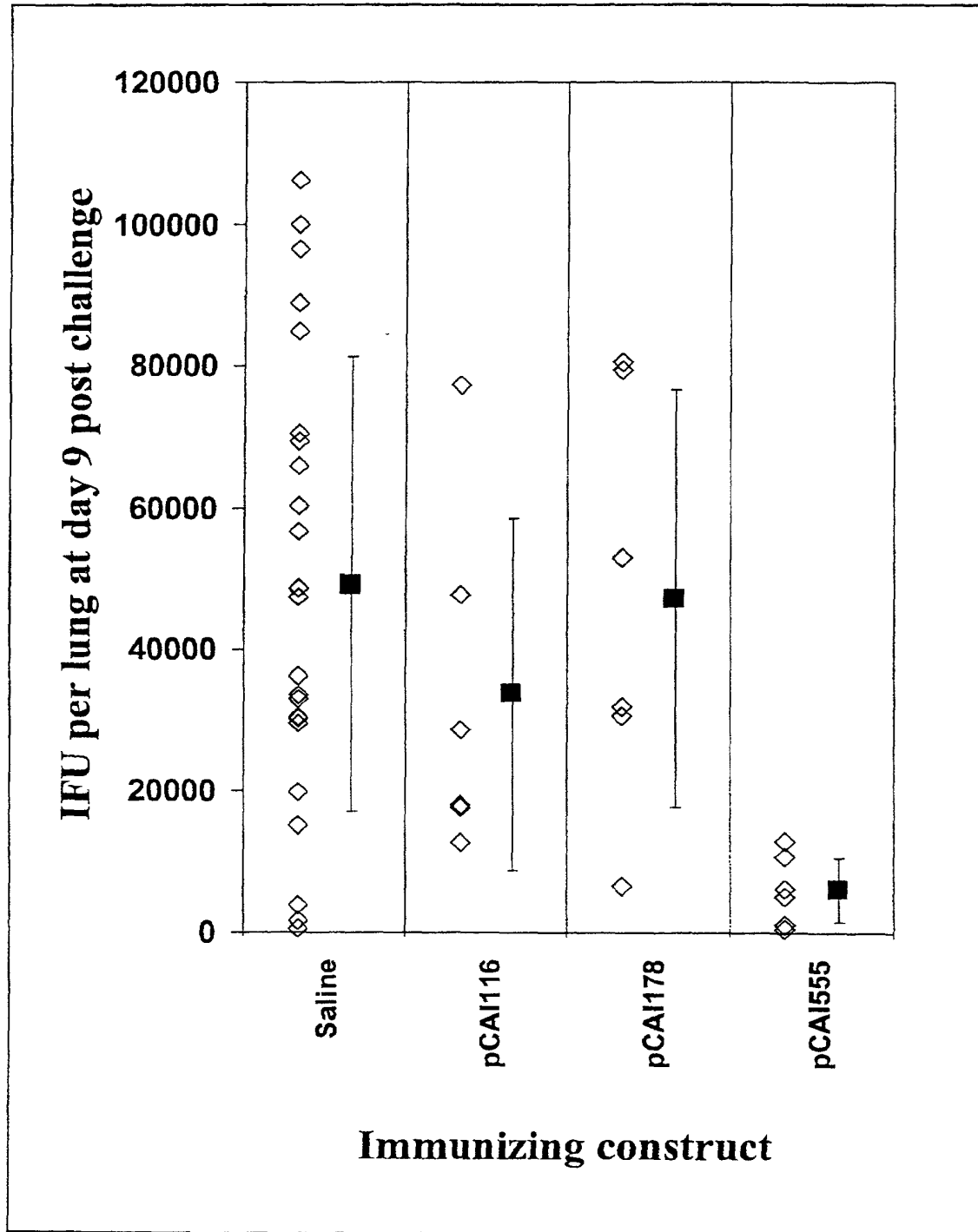
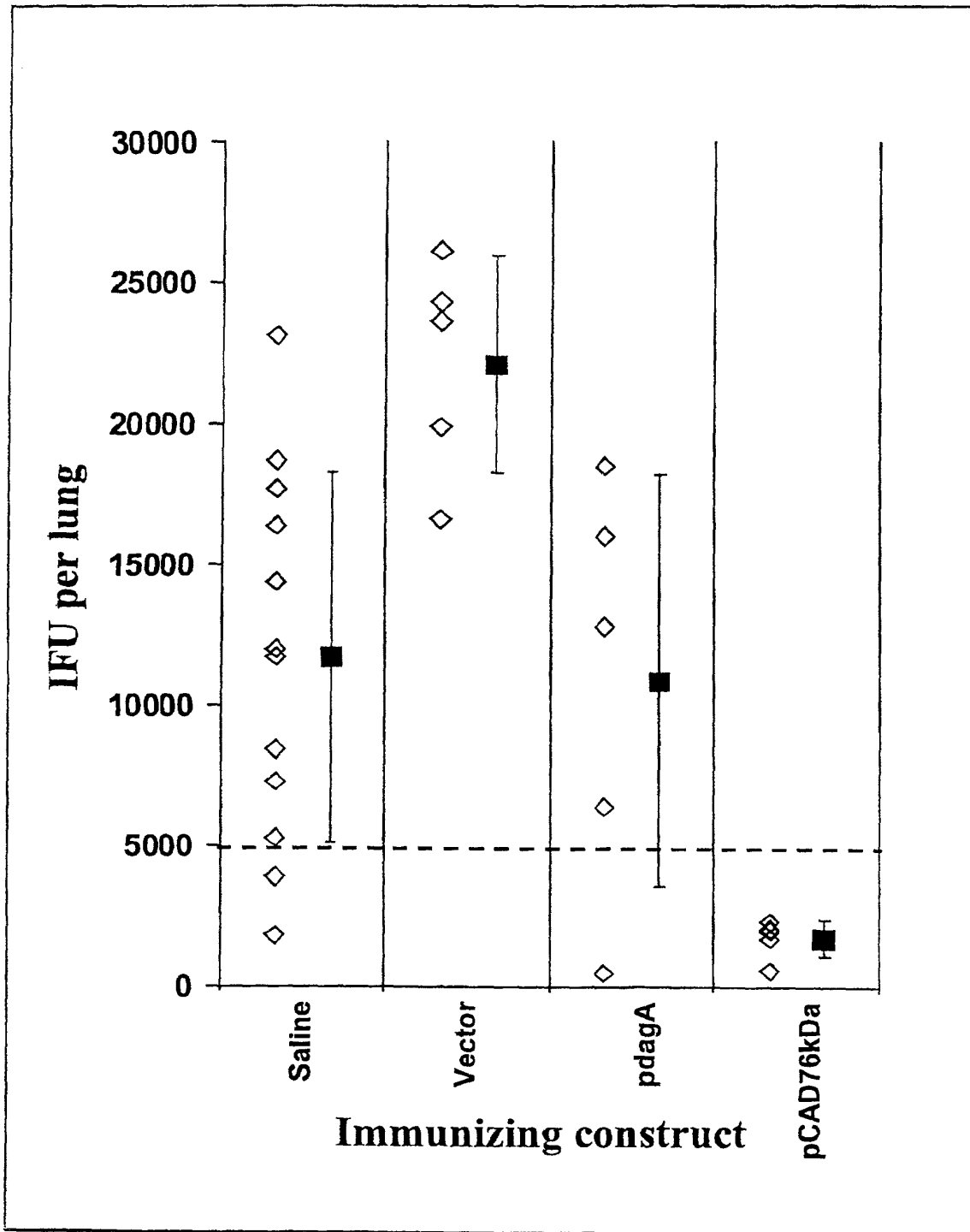


Figure 9: pCAD76kDa Confers Protection against *C. pneumoniae* Infection.



## SEQUENCE LISTING

<110> Aventis Pasteur Limited

<120> Chlamydia antigens and corresponding DNA fragments and uses thereof

<130> 77813-13

<140>

<141>

<150> US 60/132,270

<151> 1999-05-03

<150> US 60/141,276

<151> 1999-06-30

<160> 14

<170> PatentIn Ver. 2.0

<210> 1

<211> 2156

<212> DNA

<213> Chlamydia pneumoniae

<220>

<221> CDS

<222> (101)..(2053)

<400> 1

ataaaatctt taaaaacagg ctgcgattaa ttattagtga gagctttttt tttatttttt 60

ataataaaaac taaaagattt ttattatttt ttgagttttt atg gtt aat cct att 115  
Met Val Asn Pro Ile  
1 5

ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat ctt 163  
Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp Leu  
10 15 20

tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa gct 211  
Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu Ala  
25 30 35

caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc gat 259  
Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr Asp  
40 45 50

tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc atg 307  
Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu Met  
55 60 65

agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct tct 355  
Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser Ser  
70 75 80 85

act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct acg	403
Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro Thr	
90 95 100	
cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca gct	451
Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr Ala	
105 110 115	
tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct gct	499
Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala Ala	
120 125 130	
ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg gct	547
Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala Ala	
135 140 145	
act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat gcc	595
Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn Ala	
150 155 160 165	
gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat gct	643
Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr Ala	
170 175 180	
tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc ttc	691
Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser Phe	
185 190 195	
gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac aaa	739
Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn Lys	
200 205 210	
gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca ggg	787
Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro Gly	
215 220 225	
aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct aca	835
Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala Thr	
230 235 240 245	
gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat ttt	883
Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr Phe	
250 255 260	
gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat aac	931
Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn Asn	
265 270 275	
agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct aag	979
Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala Lys	
280 285 290	
aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att ctt	1027
Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile Leu	
295 300 305	



caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa aat	1075
Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys Asn	
310 315 320 325	
atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca gtt	1123
Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr Val	
330 335 340	
gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt tcc	1171
Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val Ser	
345 350 355	
atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg tct	1219
Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met Ser	
360 365 370	
ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat tct	1267
Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp Ser	
375 380 385	
caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa gcc	1315
Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys Ala	
390 395 400 405	
gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa gct	1363
Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys Ala	
410 415 420	
tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc aat	1411
Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu Asn	
425 430 435	
gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gtt cct	1459
Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val Pro	
440 445 450	
ccc gct gca gca agt tct ata ggg tca tct gta aaa cag ctt tac aag	1507
Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val Lys Gln Leu Tyr Lys	
455 460 465	
acc tca aaa tct aca ggt tct gat tat aaa aca cag ata tca gca ggt	1555
Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr Gln Ile Ser Ala Gly	
470 475 480 485	
tat gat gct tac aaa tcc atc aat gat gcc tat ggt agg gca cga aat	1603
Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ala Arg Asn	
490 495 500	
gat gcg act cgt gat gtg ata aac aat gta agt acc ccc gct ctc aca	1651
Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser Thr Pro Ala Leu Thr	
505 510 515	
cga tcc gtt cct aga gca cga aca gaa gct cga gga cca gaa aaa aca	1699
Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg Gly Pro Glu Lys Thr	
520 525 530	

4/22

gat caa gcc ctc gct agg gtg att tct ggc aat agc aga act ctt gga 1747  
 Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn Ser Arg Thr Leu Gly  
 535 540 545

gat gtc tat agt caa gtt tcg gca cta caa tct gta atg cag atc atc 1795  
 Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser Val Met Gln Ile Ile  
 550 555 560 565

cag tcg aat cct caa gcg aat aat gag gag atc aga caa aag ctt aca 1843  
 Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu Thr  
 570 575 580

tcg gca gtg aca aag cct cca cag ttt ggc tat cct tat gtg caa ctt 1891  
 Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln Leu  
 585 590 595

tct aat gac tct aca cag aag ttc ata gct aaa tta gaa agt ttg ttt 1939  
 Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu Phe  
 600 605 610

gct gaa gga tct agg aca gca gct gaa ata aaa gca ctt tcc ttt gaa 1987  
 Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe Glu  
 615 620 625

acg aac tcc ttg ttt att cag cag gtg ctg gtc aat atc ggc tct cta 2035  
 Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser Leu  
 630 635 640 645

tat tct ggt tat ctc caa taacaacacc taagtgttcg tttggagaga 2083  
 Tyr Ser Gly Tyr Leu Gln  
 650

ttattatgtg ctttggttaag gcctttgttg aggccttacc aacacactag aacgatcttc 2143

aataaataaa aga 2156

<210> 2  
 <211> 651  
 <212> PRT  
 <213> Chlamydia pneumoniae

<400> 2  
 Met Val Asn Pro Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr  
 1 5 10 15

Pro Pro Ala Asp Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn  
 20 25 30

Lys Ser Ala Glu Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys  
 35 40 45

Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala  
 50 55 60

004460-1440

5/22

Val	Asn	Ala	Leu	Met	Ser	Leu	Ala	Asp	Lys	Leu	Gly	Ile	Ala	Ser	Ser	65	70	75	80
Asn	Ser	Ser	Ser	Ser	Thr	Ser	Arg	Ser	Ala	Asp	Val	Asp	Ser	Thr	Thr	85	90	95	
Ala	Thr	Ala	Pro	Thr	Pro	Pro	Pro	Pro	Thr	Phe	Asp	Asp	Tyr	Lys	Thr	100	105	110	
Gln	Ala	Gln	Thr	Ala	Tyr	Asp	Thr	Ile	Phe	Thr	Ser	Thr	Ser	Leu	Ala	115	120	125	
Asp	Ile	Gln	Ala	Ala	Leu	Val	Ser	Leu	Gln	Asp	Ala	Val	Thr	Asn	Ile	130	135	140	
Lys	Asp	Thr	Ala	Ala	Thr	Asp	Glu	Glu	Thr	Ala	Ile	Ala	Ala	Glu	Trp	145	150	155	160
Glu	Thr	Lys	Asn	Ala	Asp	Ala	Val	Lys	Val	Gly	Ala	Gln	Ile	Thr	Glu	165	170	175	
Leu	Ala	Lys	Tyr	Ala	Ser	Asp	Asn	Gln	Ala	Ile	Leu	Asp	Ser	Leu	Gly	180	185	190	
Lys	Leu	Thr	Ser	Phe	Asp	Leu	Leu	Gln	Ala	Ala	Leu	Leu	Gln	Ser	Val	195	200	205	
Ala	Asn	Asn	Asn	Lys	Ala	Ala	Glu	Leu	Leu	Lys	Glu	Met	Gln	Asp	Asn	210	215	220	
Pro	Val	Val	Pro	Gly	Lys	Thr	Pro	Ala	Ile	Ala	Gln	Ser	Leu	Val	Asp	225	230	235	240
Gln	Thr	Asp	Ala	Thr	Ala	Thr	Gln	Ile	Glu	Lys	Asp	Gly	Asn	Ala	Ile	245	250	255	
Arg	Asp	Ala	Tyr	Phe	Ala	Gly	Gln	Asn	Ala	Ser	Gly	Ala	Val	Glu	Asn	260	265	270	
Ala	Lys	Ser	Asn	Asn	Ser	Ile	Ser	Asn	Ile	Asp	Ser	Ala	Lys	Ala	Ala	275	280	285	
Ile	Ala	Thr	Ala	Lys	Thr	Gln	Ile	Ala	Glu	Ala	Gln	Lys	Lys	Phe	Pro	290	295	300	
Asp	Ser	Pro	Ile	Leu	Gln	Glu	Ala	Glu	Gln	Met	Val	Ile	Gln	Ala	Glu	305	310	315	320
Lys	Asp	Leu	Lys	Asn	Ile	Lys	Pro	Ala	Asp	Gly	Ser	Asp	Val	Pro	Asn	325	330	335	
Pro	Gly	Thr	Thr	Val	Gly	Gly	Ser	Lys	Gln	Gln	Gly	Ser	Ser	Ile	Gly	340	345	350	

10014670-121491

6/22

Ser Ile Arg Val Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala																			
355						360					365								
Ser Ile Leu Met Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr																			
370					375					380									
Glu Asn Pro Asp Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala																			
385					390					395								400	
Arg Ala Ala Lys Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala																			
				405					410									415	
Asp Ala Gln Lys Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln																			
				420					425									430	
Gln Gly Ile Leu Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val																			
				435					440									445	
Ser Ala Gly Val Pro Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val																			
				450					455									460	
Lys Gln Leu Tyr Lys Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr																			
465					470					475									480
Gln Ile Ser Ala Gly Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr																			
				485					490										495
Gly Arg Ala Arg Asn Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser																			
				500					505									510	
Thr Pro Ala Leu Thr Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg																			
				515					520									525	
Gly Pro Glu Lys Thr Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn																			
				530					535									540	
Ser Arg Thr Leu Gly Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser																			
545					550					555									560
Val Met Gln Ile Ile Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile																			
				565					570										575
Arg Gln Lys Leu Thr Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr																			
				580					585										590
Pro Tyr Val Gln Leu Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys																			
				595					600										605
Leu Glu Ser Leu Phe Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys																			
				610					615										620
Ala Leu Ser Phe Glu Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val																			
625					630					635									640

10014570-121401

```
<210> 3
<211>
<212> DNA
<213> Chlamydia pneumoniae
<220> 1842
<221> CDS
<222> (101..(2053)
```

<400> 3																	
atg	agt	ctg	gca	gat	aag	ctg	ggt	att	gct	tct	agt	aac	agc	tcg	tct	48	
Met	Ser	Leu	Ala	Asp	Lys	Leu	Gly	Ile	Ala	Ser	Ser	Asn	Ser	Ser	Ser		
1				5				10				15					
tct	act	agc	aga	tct	gca	gac	gtg	gac	tca	acg	aca	gcg	acc	gca	cct	96	
Ser	Thr	Ser	Arg	Ser	Ala	Asp	Val	Asp	Ser	Thr	Thr	Ala	Thr	Ala	Pro		
				20				25				30					
acg	cct	cct	cca	ccc	acg	ttt	gat	gat	tat	aag	act	caa	gcg	caa	aca	144	
Thr	Pro	Pro	Pro	Pro	Thr	Phe	Asp	Asp	Tyr	Lys	Thr	Gln	Ala	Gln	Thr		
35				40				45									
gct	tac	gat	act	atc	ttt	acc	tca	aca	tca	cta	gct	gac	ata	cag	gct	192	
Ala	Tyr	Asp	Thr	Ile	Phe	Thr	Ser	Thr	Ser	Leu	Ala	Asp	Ile	Gln	Ala		
50				55				60									
gct	ttg	gtg	agc	ctc	cag	gat	gct	gtc	act	aat	ata	aag	gat	aca	gcg	240	
Ala	Leu	Val	Ser	Leu	Gln	Asp	Ala	Val	Thr	Asn	Ile	Lys	Asp	Thr	Ala		
65				70				75				80					
gct	act	gat	gag	gaa	acc	gca	atc	gct	gcg	gag	tgg	gaa	act	aag	aat	288	
Ala	Thr	Asp	Glu	Glu	Thr	Ala	Ile	Ala	Ala	Glu	Trp	Glu	Thr	Lys	Asn		
				85				90				95					
gcc	gat	gca	gtt	aaa	gtt	ggc	gcg	caa	att	aca	gaa	tta	gcg	aaa	tat	336	
Ala	Asp	Ala	Val	Lys	Val	Gly	Ala	Gln	Ile	Thr	Glu	Leu	Ala	Lys	Tyr		
100				105				110									
gct	tcg	gat	aac	caa	gcg	att	ctt	gac	tct	tta	ggc	aaa	ctg	act	tcc	384	
Ala	Ser	Asp	Asn	Gln	Ala	Ile	Leu	Asp	Ser	Leu	Gly	Lys	Leu	Thr	Ser		
115				120				125									
ttc	gac	ctc	tta	cag	gct	gct	ctt	ctc	caa	tct	gta	gca	aac	aat	aac	432	
Phe	Asp	Leu	Leu	Gln	Ala	Ala	Leu	Leu	Gln	Ser	Val	Ala	Asn	Asn	Asn		
130				135				140									
aaa	gca	gct	gag	ctt	ctt	aaa	gag	atg	caa	gat	aac	cca	gta	gtc	cca	480	
Lys	Ala	Ala	Glu	Leu	Leu	Lys	Glu	Met	Gln	Asp	Asn	Pro	Val	Val	Pro		
145				150				155				160					
ggg	aaa	acg	cct	gca	att	gct	caa	tct	tta	gtt	gat	cag	aca	gat	gct	528	
Gly	Lys	Thr	Pro	Ala	Ile	Ala	Gln	Ser	Leu	Val	Asp	Gln	Thr	Asp	Ala		
				165				170				175					

8/22

aca gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat	576
Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr	
180 190 195	
ttt gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat	624
Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn	
200 205 210	
aac agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct	672
Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala	
215 220 225	
aag aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att	720
Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile	
230 235 240 245	
ctt caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa	768
Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys	
250 255 260	
aat atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca	816
Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr	
265 270 275	
gtt gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt	864
Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val	
280 285 290	
tcc atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg	912
Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met	
295 300 305	
tct ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat	960
Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp	
310 315 320 325	
tct caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa	1008
Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys	
330 335 340	
gcc gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa	1056
Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys	
345 350 355	
gct tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc	1104
Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu	
360 365 370	
aat gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gtt	1152
Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val	
375 380 385	
Cct ccc gct gca gca agt tct ata ggg tca tct gta aaa cag ctt tac	1200
Pro Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val Lys Gln Leu Tyr	
390 395 400 405	

10014670-121401

9/22

aag acc tca aaa tct aca ggt tct gat tat aaa aca cag ata tca gca 1248  
Lys Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr Gln Ile Ser Ala  
410 415 420

ggt tat gat gct tac aaa tcc atc aat gat gcc tat ggt agg gca cga 1296  
Gly Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ala Arg  
425 430 435

aat gat gcg act cgt gat gtg ata aac aat gta agt acc ccc gct ctc 1344  
Asn Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser Thr Pro Ala Leu  
440 445 450

aca cga tcc gtt cct aga gca cga aca gaa gct cga gga cca gaa aaa 1392  
Thr Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg Gly Pro Glu Lys  
455 460 465

aca gat caa gcc ctc gct agg gtg att tct ggc aat agc aga act ctt 1440  
Thr Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn Ser Arg Thr Leu  
470 475 480 485

gga gat gtc tat agt caa gtt tcg gca cta caa tct gta atg cag atc 1488  
Gly Val Tyr Ser Gln Val Ser Ala Leu Gln Ser Val Met Gln Ile Ile  
490 495 500

act cag tcg aat cct caa gcg aat aat gag gag atc aga caa aag ctt 1536  
Ile Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu  
505 510 515

aca tcg gca gtg aca aag cct cca cag ttt ggc tat cct tat gtg caa 1584  
Thr Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln  
520 525 530

ctt tct aat gac tct aca cag aag ttc ata gct aaa tta gaa agt ttg 1632  
Leu Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu  
535 540 545

ttt gct gaa gga tct agg aca gca gct gaa ata aaa gca ctt tcc ttt 1670  
Phe Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe  
550 555 560 565

gaa acg aac tcc ttg ttt att cag cag gtg ctg gtc aat atc ggc tct 1718  
Glu Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser  
570 575 580

cta tat tct ggt tat ctc caa taacaacacc taagtgttcg tttggagaga 1769  
Leu Tyr Ser Gly Tyr Leu Gln  
585

ttattatgtg ctttggtgtaag gcctttgttg aggccttacc aacacactag aacgatcttc 1829

aataaataaaa aga 1842

10014570-121401

10/22

<210> 4

<211> 583

<212> PRT

<213> Chlamydia pneumoniae

<400> 4

Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser  
1 5 10 15  
Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro  
20 25 30  
Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr  
35 40 45  
Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala  
50 55 60  
Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala  
65 70 75 80  
Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn  
85 90 95  
Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr  
100 105 110  
Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser  
115 120 125  
Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn  
130 135 140  
Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro  
145 150 155 160  
Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala  
165 170 175  
Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr  
180 185 190  
Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn  
195 200 205  
Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala  
210 215 220  
Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile  
225 230 235 240  
Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys  
245 250 255

40044570-124401



11/22

Asn	Ile	Lys	Pro	Ala	Asp	Gly	Ser	Asp	Val	Pro	Asn	Pro	Gly	Thr	Thr	260	265	270	
Val	Gly	Gly	Ser	Lys	Gln	Gln	Gly	Ser	Ser	Ile	Gly	Ser	Ile	Arg	Val	275	280	285	
Ser	Met	Leu	Leu	Asp	Asp	Ala	Glu	Asn	Glu	Thr	Ala	Ser	Ile	Leu	Met	290	295	300	
Ser	Gly	Phe	Arg	Gln	Met	Ile	His	Met	Phe	Asn	Thr	Glu	Asn	Pro	Asp	305	310	315	320
Ser	Gln	Ala	Ala	Gln	Gln	Glu	Leu	Ala	Ala	Gln	Ala	Arg	Ala	Ala	Lys	325	330	335	
Ala	Ala	Gly	Asp	Asp	Ser	Ala	Ala	Ala	Ala	Leu	Ala	Asp	Ala	Gln	Lys	340	345	350	
Ala	Leu	Glu	Ala	Ala	Leu	Gly	Lys	Ala	Gly	Gln	Gln	Gln	Gly	Ile	Leu	355	360	365	
Asn	Ala	Leu	Gly	Gln	Ile	Ala	Ser	Ala	Ala	Val	Val	Ser	Ala	Gly	Val	370	375	380	
Pro	Pro	Ala	Ala	Ala	Ser	Ser	Ile	Gly	Ser	Ser	Val	Lys	Gln	Leu	Tyr	385	390	395	400
Lys	Thr	Ser	Lys	Ser	Thr	Gly	Ser	Asp	Tyr	Lys	Thr	Gln	Ile	Ser	Ala	405	410	415	
Gly	Tyr	Asp	Ala	Tyr	Lys	Ser	Ile	Asn	Asp	Ala	Tyr	Gly	Arg	Ala	Arg	420	425	430	
Asn	Asp	Ala	Thr	Arg	Asp	Val	Ile	Asn	Asn	Val	Ser	Thr	Pro	Ala	Leu	435	440	445	
Thr	Arg	Ser	Val	Pro	Arg	Ala	Arg	Thr	Glu	Ala	Arg	Gly	Pro	Glu	Lys	450	455	460	
Thr	Asp	Gln	Ala	Leu	Ala	Arg	Val	Ile	Ser	Gly	Asn	Ser	Arg	Thr	Leu	465	470	475	480
Gly	Asp	Val	Tyr	Ser	Gln	Val	Ser	Ala	Leu	Gln	Ser	Val	Met	Gln	Ile	485	490	495	
Ile	Gln	Ser	Asn	Pro	Gln	Ala	Asn	Asn	Glu	Glu	Ile	Arg	Gln	Lys	Leu	500	505	510	
Thr	Ser	Ala	Val	Thr	Lys	Pro	Pro	Gln	Phe	Gly	Tyr	Pro	Tyr	Val	Gln	515	520	525	
Leu	Ser	Asn	Asp	Ser	Thr	Gln	Lys	Phe	Ile	Ala	Lys	Leu	Glu	Ser	Leu	530	535	540	

10614670-13440

12/22

Phe Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe  
545 550 555 560

Glu Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser  
565 570 575

Leu Tyr Ser Gly Tyr Leu Gln  
580

<210> 5

<211> 1456

<212> DNA

<213> Chlamydia pneumoniae

<220>

<221> CDS

<222> (101)..(1456)

<400> 5

ataaaatctt taaaaacagg ctgcgattaa ttattagtga gagctttttt ttattttttt 60

ataataaaac taaaagattt ttattttttt ttgagttttt atg gtt aat cct att 115  
Met Val Asn Pro Ile  
1 5

ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat ctt 163  
Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp Leu  
10 15 20

tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa gct 211  
Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu Ala  
25 30 35

caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc gat 259  
Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr Asp  
40 45 50

tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc atg 307  
Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu Met  
55 60 65

agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct tct 355  
Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser Ser  
70 75 80 85

act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct acg 403  
Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro Thr  
90 95 100

cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca gct 451  
Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr Ala  
105 110 115

1001456-1491

tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct gct 499  
 Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala Ala  
 120 125 130

ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg gct 547  
 Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala Ala  
 135 140 145

act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat gcc 595  
 Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn Ala  
 150 155 160 165

gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat gct 643  
 Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr Ala  
 170 175 180

tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc ttc 691  
 Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser Phe  
 185 190 195

gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac aaa 739  
 Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn Lys  
 200 205 210

gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca ggg 787  
 Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro Gly  
 215 220 225

aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct aca 835  
 Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala Thr  
 230 235 240 245

gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat ttt 883  
 Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr Phe  
 250 255 260

gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat aac 931  
 Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn Asn  
 265 270 275

agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct aag 979  
 Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala Lys  
 280 285 290

aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att ctt 1027  
 Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile Leu  
 295 300 305

caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa aat 1075  
 Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys Asn  
 310 315 320 325

atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca gtt 1123  
 Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr Val  
 330 335 340

10044630-121401  
 10044630-121401

14/22

gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt tcc 1171  
Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val Ser  
345 350 355

atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg tct 1219  
Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met Ser  
360 365 370

ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat tct 1267  
Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp Ser  
375 380 385

caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa gcc 1315  
Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys Ala  
390 395 400 405

gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa gct 1363  
Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys Ala  
410 415 420

tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc aat 1411  
Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Ile Leu Asn  
425 430 435

gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gta 1456  
Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val  
440 445 450

<210> 6

<211> 452

<212> PRT

<213> Chlamydia pneumoniae

<400> 6

Met Val Asn Pro Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr  
1 5 10 15

Pro Pro Ala Asp Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn  
20 25 30

Lys Ser Ala Glu Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys  
35 40 45

Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala  
50 55 60

Val Asn Ala Leu Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser  
65 70 75 80

Asn Ser Ser Ser Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr  
85 90 95

Ala Thr Ala Pro Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr  
100 105 110

10014670-14440

15/22

Gln	Ala	Gln	Thr	Ala	Tyr	Asp	Thr	Ile	Phe	Thr	Ser	Thr	Ser	Leu	Ala	
		115						120				125				
Asp	Ile	Gln	Ala	Ala	Leu	Val	Ser	Leu	Gln	Asp	Ala	Val	Thr	Asn	Ile	
	130					135					140					
Lys	Asp	Thr	Ala	Ala	Thr	Asp	Glu	Glu	Thr	Ala	Ile	Ala	Ala	Glu	Trp	
	145				150					155					160	
Glu	Thr	Lys	Asn	Ala	Asp	Ala	Val	Lys	Val	Gly	Ala	Gln	Ile	Thr	Glu	
			165						170					175		
Leu	Ala	Lys	Tyr	Ala	Ser	Asp	Asn	Gln	Ala	Ile	Leu	Asp	Ser	Leu	Gly	
			180					185					190			
Lys	Leu	Thr	Ser	Phe	Asp	Leu	Leu	Gln	Ala	Ala	Leu	Leu	Gln	Ser	Val	
		195					200					205				
Ala	Asn	Asn	Asn	Lys	Ala	Ala	Glu	Leu	Leu	Lys	Glu	Met	Gln	Asp	Asn	
	210					215					220					
Pro	Val	Val	Pro	Gly	Lys	Thr	Pro	Ala	Ile	Ala	Gln	Ser	Leu	Val	Asp	
	225				230					235					240	
Gln	Thr	Asp	Ala	Thr	Ala	Thr	Gln	Ile	Glu	Lys	Asp	Gly	Asn	Ala	Ile	
			245						250					255		
Arg	Asp	Ala	Tyr	Phe	Ala	Gly	Gln	Asn	Ala	Ser	Gly	Ala	Val	Glu	Asn	
		260					265						270			
Ala	Lys	Ser	Asn	Asn	Ser	Ile	Ser	Asn	Ile	Asp	Ser	Ala	Lys	Ala	Ala	
		275					280					285				
Ile	Ala	Thr	Ala	Lys	Thr	Gln	Ile	Ala	Glu	Ala	Gln	Lys	Lys	Phe	Pro	
	290					295					300					
Asp	Ser	Pro	Ile	Leu	Gln	Glu	Ala	Glu	Gln	Met	Val	Ile	Gln	Ala	Glu	
	305				310					315					320	
Lys	Asp	Leu	Lys	Asn	Ile	Lys	Pro	Ala	Asp	Gly	Ser	Asp	Val	Pro	Asn	
			325						330					335		
Pro	Gly	Thr	Thr	Val	Gly	Gly	Ser	Lys	Gln	Gln	Gly	Ser	Ser	Ile	Gly	
		340						345						350		
Ser	Ile	Arg	Val	Ser	Met	Leu	Leu	Asp	Asp	Ala	Glu	Asn	Glu	Thr	Ala	
		355					360					365				
Ser	Ile	Leu	Met	Ser	Gly	Phe	Arg	Gln	Met	Ile	His	Met	Phe	Asn	Thr	
	370					375					380					
Glu	Asn	Pro	Asp	Ser	Gln	Ala	Ala	Gln	Gln	Glu	Leu	Ala	Ala	Gln	Ala	
	385				390					395					400	

10014670-1444

16/22

Arg Ala Ala Lys Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala  
405 410 415

Asp Ala Gln Lys Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln  
420 425 430

Gln Gly Ile Leu Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val  
435 440 445

Ser Ala Gly Val  
450

<210> 7  
<211> 2238  
<212> DNA  
<213> Chlamydia pneumoniae

<220>  
<221> CDS  
<222> (766)..(2235)

<400> 7  
atgacaaaaa aacattatgc ttgggttgta gaagggatc tcaatcgttt gcctaaacag 60  
ttttttgtga aatgtagtgt tgtcgactgg aacacattcg ttcttcaga aacctccact 120  
acagaaaaag ctgctacaaa cgctatgaaa tacaataact gtgtttggca gtggctcgtc 180  
ggaaagcata gtcaggttcc ttggatcaat ggacagaaaa agcctctata tctttatgga 240  
gctttcttaa tgaacccttt agcaaaggct acgaagacta cgttaaatgg aaaagaaaac 300  
ctagcttggt ttattggagg aactttaggg ggactcagaa aagctggaga ctggtctgcc 360  
acagtacgtt atgagtatgt cgaagccttg tcggttcag aaatagatgt ttcagggatt 420  
ggcctgggta atttattaaa gttttggttc gcccaagcaa ttgctgctaa ctatgatect 480  
aaagaggcta atggttttac aaattataaa ggattttccg ctctatatat gtatggcatc 540  
acagattctc tatcattcag agcttatggg gcttactcca aaccagcaaa cgataaactc 600  
ggcagtgatt ttactttccg aaagtttgat ctaggataaa ttccagcgtt ttaagtcaaa 660  
ttttaataaa atctttaaaa acaggctcgc attaattatt agtgagagct ttttttttat 720  
tttttataat aaaactaaaa gatttttatt attttttgag ttttt atg gtt aat cct 777  
Met Val Asn Pro

1

att ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat 825  
Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp  
5 10 15 20

1004460-14401

17/22

ctt tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa	873
Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu	
25 30 35	
gct caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc	921
Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr	
40 45 50	
gat tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc	969
Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu	
55 60 65	
atg agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct	1017
Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser	
70 75 80	
tct act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct	1065
Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro	
85 90 95 100	
acg cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca	1113
Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr	
105 110 115	
gct tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct	1161
Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala	
120 125 130	
gct ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg	1209
Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala	
135 140 145	
gct act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat	1257
Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn	
150 155 160	
gcc gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat	1305
Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr	
165 170 175 180	
gct tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc	1353
Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser	
185 190 195	
ttc gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac	1401
Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn	
200 205 210	
aaa gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca	1449
Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro	
215 220 225	
ggg aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct	1497
Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala	
230 235 240	

10014570-13440

aca gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat 1545  
 Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr  
 245 250 255 260

ttt gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat 1593  
 Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn  
 265 270 275

aac agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct 1641  
 Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala  
 280 285 290

aag aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att 1689  
 Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile  
 295 300 305

ctt caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa 1737  
 Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys  
 310 315 320

aat atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca 1785  
 Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr  
 325 330 335 340

gtt gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt 1833  
 Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val  
 345 350 355

tcc atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg 1881  
 Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met  
 360 365 370

tct ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat 1929  
 Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp  
 375 380 385

tct caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa 1977  
 Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys  
 390 395 400

gcc gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa 2025  
 Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys  
 405 410 415 420

gct tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc 2073  
 Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu  
 425 430 435

aat gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gta 2121  
 Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val  
 440 445 450

10014370-1440



19/22

ctc ccg ctg cag caa gtt cta tgg atc cga gct cgg tac caa gct tac 2169  
 Leu Pro Leu Gln Gln Val Leu Trp Ile Arg Ala Arg Tyr Gln Ala Tyr  
 455 460 465

gta gaa caa aaa ctc atc tca gaa gag gat ctg aat agc gcc gtc gac 2217  
 Val Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp  
 470 475 480

cat cat cat cat cat cat tga 2238  
 His His His His His His  
 485 490

<210> 8  
 <211> 490  
 <212> PRT  
 <213> Chlamydia pneumoniae

<400> 8  
 Met Val Asn Pro Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr  
 1 5 10 15

Pro Pro Ala Asp Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn  
 20 25 30

Lys Ser Ala Glu Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys  
 35 40 45

Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala  
 50 55 60

Val Asn Ala Leu Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser  
 65 70 75 80

Asn Ser Ser Ser Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr  
 85 90 95

Ala Thr Ala Pro Thr Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr  
 100 105 110

Gln Ala Gln Thr Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala  
 115 120 125

Asp Ile Gln Ala Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile  
 130 135 140

Lys Asp Thr Ala Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp  
 145 150 155 160

Glu Thr Lys Asn Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu  
 165 170 175

Leu Ala Lys Tyr Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly  
 180 185 190

10044630-134404

20/22

Lys	Leu	Thr	Ser	Phe	Asp	Leu	Leu	Gln	Ala	Ala	Leu	Leu	Gln	Ser	Val	195	200	205	
Ala	Asn	Asn	Asn	Lys	Ala	Ala	Glu	Leu	Leu	Lys	Glu	Met	Gln	Asp	Asn	210	215	220	
Pro	Val	Val	Pro	Gly	Lys	Thr	Pro	Ala	Ile	Ala	Gln	Ser	Leu	Val	Asp	225	230	235	240
Gln	Thr	Asp	Ala	Thr	Ala	Thr	Gln	Ile	Glu	Lys	Asp	Gly	Asn	Ala	Ile	245	250	255	
Arg	Asp	Ala	Tyr	Phe	Ala	Gly	Gln	Asn	Ala	Ser	Gly	Ala	Val	Glu	Asn	260	265	270	
Ala	Lys	Ser	Asn	Asn	Ser	Ile	Ser	Asn	Ile	Asp	Ser	Ala	Lys	Ala	Ala	275	280	285	
Ile	Ala	Thr	Ala	Lys	Thr	Gln	Ile	Ala	Glu	Ala	Gln	Lys	Lys	Phe	Pro	290	295	300	
Asp	Ser	Pro	Ile	Leu	Gln	Glu	Ala	Glu	Gln	Met	Val	Ile	Gln	Ala	Glu	305	310	315	320
Lys	Asp	Leu	Lys	Asn	Ile	Lys	Pro	Ala	Asp	Gly	Ser	Asp	Val	Pro	Asn	325	330	335	
Pro	Gly	Thr	Thr	Val	Gly	Gly	Ser	Lys	Gln	Gln	Gly	Ser	Ser	Ile	Gly	340	345	350	
Ser	Ile	Arg	Val	Ser	Met	Leu	Leu	Asp	Asp	Ala	Glu	Asn	Glu	Thr	Ala	355	360	365	
Ser	Ile	Leu	Met	Ser	Gly	Phe	Arg	Gln	Met	Ile	His	Met	Phe	Asn	Thr	370	375	380	
Glu	Asn	Pro	Asp	Ser	Gln	Ala	Ala	Gln	Gln	Glu	Leu	Ala	Ala	Gln	Ala	385	390	395	400
Arg	Ala	Ala	Lys	Ala	Ala	Gly	Asp	Asp	Ser	Ala	Ala	Ala	Ala	Leu	Ala	405	410	415	
Asp	Ala	Gln	Lys	Ala	Leu	Glu	Ala	Ala	Leu	Gly	Lys	Ala	Gly	Gln	Gln	420	425	430	
Gln	Gly	Ile	Leu	Asn	Ala	Leu	Gly	Gln	Ile	Ala	Ser	Ala	Ala	Val	Val	435	440	445	
Ser	Ala	Gly	Val	Leu	Pro	Leu	Gln	Gln	Val	Leu	Trp	Ile	Arg	Ala	Arg	450	455	460	
Tyr	Gln	Ala	Tyr	Val	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	465	470	475	480

10014670-4804

```
<210> 9
<211> 43
<212> DNA
<213> primer
```

ataagaatgc ggccgccacc atggttaatc ctattggtcc agg 43

<400> 10

gcgccggatc ccttggagat aaccagaata tagag 35

<400> 11

ataagaatgc ggccgccacc atgagtctgg cagataagct ggg 43

<400> 12

gcgccggatc ccttggagat aaccagaata ta 32

<400> 13

gctctagacc gccatgacaa aaaaacatta tgcttggg 38

22/22

<210> 14  
<211> 28  
<212> DNA  
<213> primer

<400> 14

cgggatccat agaacttgct gcagcggg

28

100344570-121401